

## SEQUENCE LISTING

<110> Jones, David HA  
Bout, Abraham

<120> Efficient Production of IgA in Recombinant Mammalian Cells

<130> 2578-6077

<150> US 09/549,463  
<151> 2000-04-14

<150> US 60/129,452  
<151> 1999-04-15

<160> 8

<170> PatentIn version 3.2

<210> 1  
<211> 2022  
<212> DNA  
<213> Artificial

<220>

<223> Genomic DNA encoding heavy chain of anti-EpCAM IgA

<220>  
<221> misc\_feature  
<222> (1)..(3)  
<223> Start codon

<220>  
<221> misc\_feature  
<222> (2020)..(2022)  
<223> Stop codon

<400> 1

atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgttttga atttccatg 60

gcccgaggc agctggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgagg 120

gtctcctgca aggcttctgg aggcacccctc agcagctatg ctatcagctg ggtgcgcacag 180

gccccctggac aagggcgttga gtggatggga gggatcatcc ctatcttgg tacagcaa 240  
tacgcacaga agttccaggg cagagtcacg attaccgcgg acgaatccac gagcacagcc 300  
tacatggagc tgagcagcct gagatcttag gacacggctg tgtattactg tgcaagagac 360  
cggtttcttc actattgggg ccaaggtaacc ctggtcaccg tctcgacagg tgagtgcggc 420  
cgctctgtgc tgggttcctc cagtatagag gagaggcagg cacagactgt cctcctgggg 480  
acatggcatg agggccgcgt cctcacagtg cattctgtgt tccagcatcc ccgaccagcc 540  
ccaaggctt cccgctgagc ctctgcagca cccagccaga tgggaacgtg gtcatgcct 600  
gcctggtcca gggcttcttc ccccaggagc cactcagtgt gacctggagc gaaagcggac 660  
agggcgtgac cgccagaaac ttcccaccca gccaggatgc ctccggggac ctgtacacca 720  
cgagcagcca gctgaccctg ccggccacac agtgccttagc cggcaagtcc gtgacatgcc 780  
acgtgaagca ctacacgaat cccagccagg atgtgactgt gccctgccc ggtcagaggg 840  
caggctgggg agtggggcgg ggccaccccg tcgtgccctg acactgegcc tgccacccgtg 900  
ttccccacag ggagccgccc cttcactcac accagagtgg accgcggggcc gagccccagg 960  
aggtggtggt ggacaggcca ggaggggcga ggccggggca tgggaagca tgtgctgacc 1020  
agctcaggcc atctctccac tccagttccc tcaactccac ctacccatc tccctcaact 1080  
ccacctaccc catctccctc atgctgccac ccccgactgt cactgcaccg accggccctc 1140  
gaggacctgc tcttaggttc agaagcgaac ctcacgtca cactgaccgg cctgagagat 1200  
gcctcaggtg tcacccatc ctggacgccc tcaagtggga agagcgctgt tcaaggacca 1260  
cctgaccgtg acctctgtgg ctgctacagc gtgtccagtg tccgtcggg ctgtgccgag 1320  
ccatggacc atgggaagac cttcacttgc actgctgcct accccgagtc caagaccccg 1380  
ctaaccgcca ccctctcaaa atccgggtggg tccagaccct gctcggggcc ctgctcagt 1440  
ctctggttt caaagcatat tcctggcctg ctcctccct cccaatcctg ggctccagtg 1500  
ctcatgccaa gtacagaggg aaactgaggc aggctgaggg gccaggacac agcccggtt 1560

gccaccaga gcagagggc tctctatcc cctgcccagc cccctgacct ggctctac 1620  
cctccaggaa acacattcg gcccgggtc cacctgctgc cgccggcgtc ggaggagctg 1680  
gccctgaacg agctggtgac gctgacgtgc ctggcacgtg gcttcagccc caaggatgtg 1740  
ctggttcgct ggctgcagg gtcacaggag ctgccccgca agaagtacct gacttggca 1800  
tcccggcagg agcccgcca gggcaccacc accttcgctg tgaccagcat actgcgcgtg 1860  
gcagccgagg actggaagaa gggggacacc ttctcctgca tggtggcca cgaggccctg 1920  
ccgctggct tcacacagaa gaccatcgac cgcttggcgg gtaaacccac ccatgtcaat 1980  
gtgtctgttg tcatggcggaa ggtggacggc acctgctact ga 2022

<210> 2  
<211> 922  
<212> DNA  
<213> Artificial

<220>  
<223> Genomic DNA encoding light chain of anti-EpCAM IgA

<220>  
<221> misc\_feature  
<222> (1)..(3)  
<223> Start Codon

<220>  
<221> misc\_feature  
<222> (920)..(922)  
<223> Stop Codon

<400> 2  
atggcatgcc ctggcttcct gtggcacatt gtgatctcca cctgtcttga atttccatg 60  
gctgaaattg agctcactca gtctccactc tccctgcccgtc acaccctgg agagccggcc 120  
tccatctcct gcaggtcttag tcagagccctc ctgcatacgta atggatacaa ctatttggat 180  
tggtacctgc agaagccagg gcagtcctca cagtcctga tctatttggg ttctaattcgg 240

gcctccgggg tccctgacag gttcagtggc agtggatcg gcacagatt tacactgaaa 300  
atcagcagag tggaggctga ggatgtggg gtttattact gcatgcaagc tctacaaact 360  
ttcacttcg gccctggac caaggtggag atcaaacgta agtgcactt gcggccgcta 420  
ggaagaaaact caaaacatca agatttaaa tacgcttcg ggtctccttg ctataattat 480  
ctggataag catgctgtt tctgtctgtc cctaacatgc cctgtgatta tccgcaaaca 540  
acacacccaa gggcagaact ttgttactta aacaccatcc tgttgcttc ttcctcagg 600  
aactgtggct gcaccatctg tcttcattt cccgccccatct gatgagcagt tgaaatctgg 660  
aactgcctct gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagt 720  
gaaggtggat aacgcccctcc aatcgggtaa ctcccaggag agtgcacag agcaggacag 780  
caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa 840  
acacaaagtc tacgcctgcg aagtccacca tcagggcctg agctcgcccg tcacaaagag 900  
cttcaacagg ggagagtgtt ag 922

<210> 3  
<211> 489  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence anti-EpCAM IgA heavy chain

<220>  
<221> MISC\_FEATURE  
<222> (1)..(21)  
<223> leader peptide

<220>  
<221> MISC\_FEATURE  
<222> (22)..(136)  
<223> VH Region

<220>  
<221> MISC\_FEATURE  
<222> (137)..(238)  
<223> CH1 Region

<220>  
<221> MISC\_FEATURE  
<222> (239)..(359)  
<223> CH2 Region

<220>  
<221> MISC\_FEATURE  
<222> (360)..(489)  
<223> CH3 Region

<400> 3

Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu  
1           5           10           15

Glu Phe Ser Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val  
20           25           30

Lys Lys Pro Gly Ser Ser Val Arg Val Ser Cys Lys Ala Ser Gly Gly  
35           40           45

Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln  
50           55           60

Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn  
65           70           75           80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser  
85           90           95

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr  
100           105           110

Ala Val Tyr Tyr Cys Ala Arg Asp Pro Phe Leu His Tyr Trp Gly Gln  
115           120           125

Gly Thr Leu Val Thr Val Ser Thr Ala Ser Pro Thr Ser Pro Lys Val  
130           135           140

Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp Gly Asn Val Val Ile

145            150            155            160  
Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr  
165            170            175  
  
Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg Asn Phe Pro Pro Ser  
180            185            190  
  
Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu  
195            200            205  
  
Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val Thr Cys His Val Lys  
210            215            220  
  
His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val Pro Cys Pro Val Pro  
225            230            235            240  
  
Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro  
245            250            255  
  
Ser Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp  
260            265            270  
  
  
Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu  
275            280            285  
  
Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys  
290            295            300  
  
Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser  
305            310            315            320  
  
Val Ser Ser Val Leu Ser Gly Cys Ala Glu Pro Trp Asn His Gly Lys  
325            330            335  
  
Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr  
340            345            350  
  
Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu  
355            360            365  
  
Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu  
370            375            380

Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp  
385            390            395            400

Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala  
405            410            415

Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser  
420            425            430

Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser  
435            440            445

Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr  
450            455            460

Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val  
465            470            475            480

Met Ala Glu Val Asp Gly Thr Cys Tyr  
485

<210> 4

<211> 239

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence anti-EpCAM IgA light chain

<220>

<221> MISC\_FEATURE

<222> (1)..(21)

<223> leader peptide

<220>

<221> MISC\_FEATURE

<222> (22)..(132)

<223> VL region

<220>

<221> MISC\_FEATURE

<222> (133)..(239)

<223> CL region

<400> 4

Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu  
1 5 10 15

Glu Phe Ser Met Ala Glu Ile Glu Leu Thr Gln Ser Pro Leu Ser Leu  
20 25 30

Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln  
35 40 45

Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln  
50 55 60

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg  
65 70 75 80

Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr  
100 105 110

Tyr Cys Met Gln Ala Leu Gln Thr Phe Thr Phe Gly Pro Gly Thr Lys  
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
180                185                190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
195                200                205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
210                215                220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225                230                235

<210> 5  
<211> 38  
<212> DNA  
<213> Artificial

<220>  
<223> E001 forward primer for amplification of light chain

<400> 5  
cctggcgcc caccatggca tgccctggct tcctgtgg                38

<210> 6  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> E002 reverse primer for amplification of light chain

<400> 6  
ccgggttaac taacactctc ccctgttcaa gc                32

<210> 7  
<211> 39  
<212> DNA  
<213> Artificial

<220>

<223> E003 forward primer for amplification of heavy chain

<400> 7

ggaggatccg ccaccatggc atgcctggc ttccgtgg 39

<210> 8

<211> 29

<212> DNA

<213> Artificial

<220>

<223> P01 reverse primer for amplification of heavy chain

<400> 8

ggaccgctag ctcagtagca ggtgccgac 29